GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 19:39:12 ; Search time 142 Seconds
(without alignments)
27.987 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKYAESD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 252723

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	51.9	13	14	US-10-199-869-23	Sequence 23, Appl
2	26	48.1	13	15	US-10-308-128-29	Sequence 29, Appl
3	26	48.1	15	14	US-10-210-428-25	Sequence 25, Appl
4	26	48.1	15	17	US-10-882-074-25	Sequence 25, Appl
5	25	46.3	12	14	US-10-084-813-925	Sequence 925, App
6	25	46.3	12	14	US-10-084-813-926	Sequence 926, App
7	25	46.3	14	9	US-09-999-699-7	Sequence 7, Appli
8	25	46.3	15	14	US-10-084-813-689	Sequence 689, App
9	25	46.3	15	14	US-10-084-813-690	Sequence 690, App
10	25	46.3	15	14	US-10-084-813-691	Sequence 691, App
11	25	46.3	15	14	US-10-084-813-692	Sequence 692, App
12	25	46.3	15	14	US-10-084-813-693	Sequence 693, App
13	24	44.4	14	17	US-10-474-298-19	Sequence 19, Appl
14	24	44.4	14	17	US-10-474-298-23	Sequence 23, Appl
15	23	42.6	6	17	US-10-654-578-1897	Sequence 1897, Ap
16	23	42.6	10	14	US-10-190-082-380	Sequence 380, App
17	23	42.6	12	9	US-09-848-664-5	Sequence 5, Appli
18	23	42.6	12	14	US-10-190-082-387	Sequence 387, App
19	23	42.6	12	16	US-10-652-407-58	Sequence 58, Appl
20	23	42.6	13	10	US-09-201-396-2	Sequence 2, Appli
21	23	42.6	13	10	US-09-965-536A-37	Sequence 37, Appl
22	23	42.6	13	14	US-10-277-607-2	Sequence 2, Appli
23	23	42.6	14	17	US-10-865-478-847	Sequence 847, App
24	23	42.6	15	14	US-10-231-894-34	Sequence 34, Appl
25	23	42.6	15	14	US-10-231-889-34	Sequence 34, Appl
26	23	42.6	15	15	US-10-224-268-3	Sequence 3, Appli
27	23	42.6	15	15	US-10-644-703-6	Sequence 6, Appli
28	23	42.6	15	17	US-10-641-633-52	Sequence 52, Appl
29	22	40.7	6	14	US-10-106-804B-14	Sequence 14, Appl
30	22	40.7	6	14	US-10-323-046-16	Sequence 16, Appl
31	22	40.7	6	17	US-10-654-578-1564	Sequence 1564, Ap
32	22	40.7	7	14	US-10-006-869-3417	Sequence 3417, Ap
33	22	40.7	7	14	US-10-006-869-3432	Sequence 3432, Ap
34	22	40.7	7	14	US-10-006-869-3501	Sequence 3501, Ap
35	22	40.7	7	14	US-10-006-869-3516	Sequence 3516, Ap
36	22	40.7	7	14	US-10-190-082-644	Sequence 644, App
37	22	40.7	7	14	US-10-395-032-3417	Sequence 3417, Ap
38	22	40.7	7	14	US-10-395-032-3432	Sequence 3432, Ap
39	22	40.7	7	14	US-10-395-032-3501	Sequence 3501, Ap
40	22	40.7	7	14	US-10-395-032-3516	Sequence 3516, Ap
41	22	40.7	7	17	US-10-654-578-761	Sequence 761, App
42	22	40.7	7	17	US-10-654-578-776	Sequence 776, App
43	22	40.7	7	17	US-10-654-578-845	Sequence 845, App
44	22	40.7	7	17	US-10-654-578-860	Sequence 860, App
45	22	40.7	8	14	US-10-006-869-3418	Sequence 3418, Ap
46	22	40.7	8	14	US-10-006-869-3433	Sequence 3433, Ap
47	22	40.7	8	14	US-10-006-869-3502	Sequence 3502, Ap
48	22	40.7	8	14	US-10-006-869-3517	Sequence 3517, Ap
49	22	40.7	8	14	US-10-395-032-3418	Sequence 3418, Ap
50	22	40.7	8	14	US-10-395-032-3433	Sequence 3433, Ap

ALIGNMENTS

RESULT 1
US-10-199-869-23
; Sequence 23, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SU
; TITLE OF INVENTION: K+alphaM2
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-869-23

Query Match 51.9%; Score 28; DB 14; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 FRSLKYAES 10
              ||| :|: |
Db          4 FRSARYSRS 12
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RESULT 2

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 19:30:31 ; Search time 38 Seconds
(without alignments)
19.197 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKYAESD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	51.9	6	3	US-09-360-237-13	Sequence 13, Appl
2	28	51.9	8	3	US-09-360-237-14	Sequence 14, Appl
3	25	46.3	9	1	US-08-185-448-9	Sequence 9, Appli
4	25	46.3	14	2	US-08-883-070-4	Sequence 4, Appli
5	25	46.3	14	4	US-09-999-699-7	Sequence 7, Appli
6	23	42.6	6	4	US-09-535-852-1897	Sequence 1897, Ap
7	23	42.6	7	1	US-08-082-847-17	Sequence 17, Appl
8	23	42.6	8	1	US-08-082-847-7	Sequence 7, Appli
9	23	42.6	8	1	US-08-082-847-9	Sequence 9, Appli
10	23	42.6	8	1	US-08-082-847-29	Sequence 29, Appl
11	23	42.6	8	4	US-09-680-571A-84	Sequence 84, Appl
12	23	42.6	8	4	US-09-680-571A-86	Sequence 86, Appl
13	23	42.6	9	1	US-08-082-847-31	Sequence 31, Appl
14	23	42.6	9	1	US-08-082-847-32	Sequence 32, Appl
15	23	42.6	9	1	US-08-082-847-35	Sequence 35, Appl
16	23	42.6	9	1	US-08-082-847-36	Sequence 36, Appl
17	23	42.6	10	1	US-07-830-330-13	Sequence 13, Appl
18	23	42.6	10	1	US-08-082-847-19	Sequence 19, Appl
19	23	42.6	10	1	US-08-082-847-21	Sequence 21, Appl
20	23	42.6	10	1	US-08-133-271-6	Sequence 6, Appli
21	23	42.6	10	3	US-08-855-958-1	Sequence 1, Appli
22	23	42.6	10	3	US-08-855-958-7	Sequence 7, Appli
23	23	42.6	10	3	US-08-855-958-8	Sequence 8, Appli
24	23	42.6	11	3	US-08-855-958-4	Sequence 4, Appli
25	23	42.6	11	3	US-08-855-958-9	Sequence 9, Appli
26	23	42.6	12	4	US-09-848-664A-5	Sequence 5, Appli
27	23	42.6	13	1	US-07-830-330-14	Sequence 14, Appl
28	23	42.6	15	1	US-07-830-330-15	Sequence 15, Appl
29	23	42.6	15	1	US-08-133-271-1	Sequence 1, Appli
30	23	42.6	15	3	US-09-045-632-105	Sequence 105, App
31	23	42.6	15	3	US-08-855-958-5	Sequence 5, Appli
32	22	40.7	6	1	US-08-082-847-4	Sequence 4, Appli
33	22	40.7	6	1	US-08-393-305-15	Sequence 15, Appl
34	22	40.7	6	1	US-08-726-817-15	Sequence 15, Appl
35	22	40.7	6	2	US-08-725-969-15	Sequence 15, Appl
36	22	40.7	6	2	US-08-794-524-15	Sequence 15, Appl
37	22	40.7	6	3	US-09-189-193-15	Sequence 15, Appl
38	22	40.7	6	3	US-09-360-237-41	Sequence 41, Appl
39	22	40.7	6	4	US-09-675-922-16	Sequence 16, Appl
40	22	40.7	6	4	US-09-535-852-1564	Sequence 1564, Ap
41	22	40.7	7	1	US-08-082-847-15	Sequence 15, Appl
42	22	40.7	7	1	US-08-082-847-16	Sequence 16, Appl
43	22	40.7	7	1	US-08-082-847-18	Sequence 18, Appl
44	22	40.7	7	3	US-09-360-237-32	Sequence 32, Appl
45	22	40.7	7	3	US-09-187-859-3417	Sequence 3417, Ap
46	22	40.7	7	3	US-09-187-859-3432	Sequence 3432, Ap
47	22	40.7	7	3	US-09-187-859-3501	Sequence 3501, Ap
48	22	40.7	7	3	US-09-187-859-3516	Sequence 3516, Ap
49	22	40.7	7	4	US-09-839-542B-3417	Sequence 3417, Ap
50	22	40.7	7	4	US-09-839-542B-3432	Sequence 3432, Ap

ALIGNMENTS

RESULT 1
US-09-360-237-13
; Sequence 13, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-13

Query Match 51.9%; Score 28; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VFRSLK 6
||||||
Db 1 VFRSLK 6

RESULT 2
US-09-360-237-14
; Sequence 14, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 19:22:00 ; Search time 191 Seconds
(without alignments)
33.137 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKYAESD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	44.4	15	2	Q7M1X0	Q7m1x0 arabidopsis
2	23	42.6	15	2	Q86128	Q86128 vesicular s
3	22	40.7	11	2	Q8NI03	Q8ni03 homo sapien
4	22	40.7	14	2	Q8S2V1	Q8s2v1 zea mays (m
5	22	40.7	15	2	Q8S2V2	Q8s2v2 zea mays (m
6	20	37.0	10	2	Q71VB8	Q71vb8 homo sapien
7	20	37.0	10	2	AAB82538	Aab82538 homo sapi
8	19	35.2	8	2	Q9GD00	Q9gd00 masoala mad
9	19	35.2	10	1	UXA6_CHLTR	P38007 chlamydia t
10	19	35.2	10	2	Q7M2Z8	Q7m2z8 bos taurus
11	19	35.2	10	2	Q9F5W1	Q9f5w1 vibrio chol
12	19	35.2	11	2	P77404	P77404 escherichia
13	19	35.2	13	2	Q7RAS8	Q7ras8 plasmodium
14	19	35.2	13	2	Q33417	Q33417 digitalis p
15	19	35.2	13	2	Q9MQK6	Q9mqk6 rupicapra r
16	19	35.2	15	2	O99386	O99386 sus scrofa
17	18	33.3	6	2	P82541	P82541 spinacia ol
18	18	33.3	8	2	Q7GEF5	Q7gef5 nicotiana b
19	18	33.3	8	2	Q36898	Q36898 nicotiana p
20	18	33.3	9	2	Q7M1V3	Q7m1v3 oryza sativ
21	18	33.3	11	2	Q32704	Q32704 nicotiana t
22	18	33.3	11	2	Q6LDR1	Q6ldr1 salmonella
23	18	33.3	11	2	AAA99292	Aaa99292 salmonell
24	18	33.3	14	2	Q71UL1	Q71ul1 haliotis ru
25	18	33.3	14	2	AAC35347	Aac35347 haliotis
26	18	33.3	14	2	AAC35345	Aac35345 haliotis
27	18	33.3	15	1	MILT_ONCKE	P81037 oncorhynchu
28	18	33.3	15	2	Q7M4Z6	Q7m4z6 fusarium sp
29	18	33.3	15	2	Q9BZN0	Q9bzn0 homo sapien
30	18	33.3	15	2	Q7R923	Q7r923 plasmodium
31	18	33.3	15	2	Q7RBW7	Q7rbw7 plasmodium
32	18	33.3	15	2	Q9TRL0	Q9trl0 canis famil
33	18	33.3	15	2	Q9TNQ5	Q9tnq5 mus sp. maj
34	18	33.3	15	2	Q7GEF3	Q7gef3 nicotiana g
35	18	33.3	15	2	Q7GEF4	Q7gef4 nicotiana t
36	18	33.3	15	2	Q37016	Q37016 nicotiana a
37	18	33.3	15	2	Q9XGM5	Q9xgm5 arabidopsis
38	18	33.3	15	2	Q798N7	Q798n7 streptococc
39	18	33.3	15	2	CAB01929	Cab01929 streptoco
40	17	31.5	13	1	AU11_LITRA	P82386 litoria ran
41	17	31.5	13	1	AU12_LITRA	P82387 litoria ran
42	17	31.5	13	2	P82560	P82560 streptococc
43	17	31.5	13	2	P82808	P82808 rattus norv
44	17	31.5	15	2	Q8WK21	Q8wk21 bolidomonas
45	17	31.5	15	2	Q9S8M9	Q9s8m9 raphanus sa
46	17	31.5	15	2	Q53541	Q53541 bacillus sp
47	17	31.5	15	2	Q6LCW3	Q6lcw3 mus musculu
48	17	31.5	15	2	Q88954	Q88954 vaccinia vi
49	17	31.5	15	2	Q9IBM5	Q9ibm5 human immun
50	17	31.5	15	2	AAA85677	Aaa85677 mus muscu

ALIGNMENTS

RESULT 1
Q7M1X0
ID Q7M1X0 PRELIMINARY; PRT; 15 AA.
AC Q7M1X0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glycine cleavage system protein H1 and H2 (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE.
RA Kamo M., Kawakami T., Miyatake N., Tsugita A.;
RL Submitted (JUL-1994) to the PIR data bank.
DR PIR; PA0036; PA0036.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1750 MW; 5A50DFA18A83898C CRC64;

Query Match 44.4%; Score 24; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 VFRSLKYA 8
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Db          3 VLEGLKYA 10
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RESULT 2
Q86128
ID Q86128 PRELIMINARY; PRT; 15 AA.
AC Q86128;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE N protein (Fragment).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80001959; PubMed=89911;
RA Mcgeoch D.J.;
RT "Structure of the gene N: gene NS intercistronic junction in the
RT genome of vesicular stomatitis virus.";

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 19:22:45 ; Search time 39 Seconds
(without alignments)
27.138 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKYAESD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	44.4	15	2	PA0036	glycine cleavage s
2	19	35.2	10	2	JC1367	thyroliberin poten
3	19	35.2	11	2	A26930	ermG leader peptid
4	18	33.3	9	2	PS0253	glycine cleavage s
5	18	33.3	10	2	PT0322	Ig heavy chain CRD
6	18	33.3	11	2	PC2372	58K heat shock pro
7	18	33.3	11	2	B29806	acidic proline-ric
8	18	33.3	15	2	PA0093	enniatin synthetas
9	18	33.3	15	2	B45133	casein kinase II (
10	17	31.5	11	2	I54193	Rhesus blood group
11	17	31.5	12	2	PH1611	Ig H chain V-D-J r
12	17	31.5	15	2	JN0730	hypothetical 1.7K
13	16	29.6	7	2	S17976	glucose isomerase
14	16	29.6	8	2	S45651	probable Na+-trans
15	16	29.6	8	2	S37141	rpsA protein - Erw
16	16	29.6	9	2	A44873	caldesmon - rabbit
17	16	29.6	9	2	PT0324	Ig heavy chain CRD
18	16	29.6	9	2	S02384	probable membrane
19	16	29.6	9	2	PC7073	ubiquinol-cytochro
20	16	29.6	10	2	S77990	cytochrome-c oxida
21	16	29.6	11	2	PH0914	T-cell receptor be
22	16	29.6	12	2	PH0936	T-cell receptor be
23	16	29.6	13	2	PT0290	Ig heavy chain CRD
24	16	29.6	13	2	H56046	urinary tract ston
25	16	29.6	14	1	LFECFS	pheST operon leade
26	16	29.6	14	2	F90931	pheST operon leade
27	16	29.6	14	2	B85780	pheST operon leade
28	16	29.6	14	2	I64815	carbonic anhydrase
29	16	29.6	14	2	AG0705	phenylalanyl-tRNA
30	16	29.6	14	2	AF0296	phenylalanyl-tRNA
31	16	29.6	15	2	PA0086	protein QF200044 -
32	16	29.6	15	2	PA0099	phenotipic variati
33	16	29.6	15	2	PA0059	protein QF200021 -
34	16	29.6	15	2	S04586	NADH2 dehydrogenas
35	15	27.8	10	2	S65728	hemoglobin, extrac
36	15	27.8	10	2	A44871	monodehydroascorba
37	15	27.8	10	2	GXHU1	gastric juice pept
38	15	27.8	11	2	S66606	quinoline 2-oxidor
39	15	27.8	12	2	PQ0730	unidentified 5.4/3
40	15	27.8	13	2	S41209	F420-non-reducing-
41	15	27.8	13	2	E60396	antigen 7H8/2 - ma
42	15	27.8	13	2	I54984	aeg-46.5 protein -
43	15	27.8	14	2	I54284	C1-inhibitor - hum
44	15	27.8	14	2	B28018	very late antigen-
45	15	27.8	14	2	I49514	B144 protein A - m
46	15	27.8	14	2	PC4376	telomeric and tetr
47	15	27.8	14	2	S68095	calcium-binding pr
48	15	27.8	15	2	A60834	angiotensin I prec
49	15	27.8	15	2	S13973	chlorophyll a/b-bi
50	15	27.8	15	2	S62620	protein disulfide-

ALIGNMENTS

RESULT 1
PA0036
glycine cleavage system protein H1 and H2 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: PA0036
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensior
A;Reference number: PA0001
A;Accession: PA0036
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Cross-references: UNIPROT:Q7M1X0
A;Experimental source: stem

Query Match 44.4%; Score 24; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 VFRSLKYA 8
              |   ||||
Db          3 VLEGLKYA 10
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RESULT 2
JC1367
thyroliberin potentiating neuropeptide - bovine
N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiating
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1367
R;Bulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.
Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992
A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovine
A;Reference number: JC1367; MUID:93111999; PMID:1472021
A;Accession: JC1367
A;Molecule type: protein
A;Residues: 1-10 <BUL>
A;Cross-references: UNIPROT:Q7M2Z8
A;Experimental source: hypothalamus
C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precursor
C;Function:
A;Description: potentiates thyroliberin-induced thyrotropin secretion
C;Superfamily: thyroliberin
C;Keywords: hypothalamus; neuropeptide

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 27, 2005, 19:21:20 ; Search time 156 Seconds
(without alignments)
25.295 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKYAESD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	11	3	AAB06265	Aab06265 Subtilisi
2	54	100.0	13	3	AAB06266	Aab06266 Subtilisi
3	54	100.0	14	3	AAB06329	Aab06329 Synthetic
4	54	100.0	15	3	AAB06325	Aab06325 Human sub
5	54	100.0	15	3	AAB06289	Aab06289 Synthetic
6	44	81.5	12	3	AAB06330	Aab06330 Synthetic
7	28	51.9	6	3	AAY84192	Aay84192 Peptide s
8	28	51.9	6	4	AAB97409	Aab97409 Site-1 pr
9	28	51.9	6	4	AAB97420	Aab97420 Site-1 pr
10	28	51.9	8	3	AAB06285	Aab06285 Human SKI
11	28	51.9	8	3	AAY84230	Aay84230 Amino aci
12	28	51.9	8	3	AAY84193	Aay84193 Peptide s
13	28	51.9	8	4	AAB97403	Aab97403 Site-1 pr
14	28	51.9	13	7	ADJ79884	Adj79884 Human pot
15	27	50.0	12	4	AAM98241	Aam98241 Human pep
16	27	50.0	15	4	AAG64901	Aag64901 Human kin
17	26	48.1	9	6	ABR13967	Abr13967 Human can
18	26	48.1	9	6	ABR14446	Abr14446 Human can
19	26	48.1	9	6	ABR13833	Abr13833 Human can
20	26	48.1	9	6	ABR14242	Abr14242 Human can
21	26	48.1	9	6	ABR13662	Abr13662 Human can
22	26	48.1	10	3	AAB10157	Aab10157 ISS1/1 Po
23	26	48.1	10	4	AAB75671	Aab75671 HLA class
24	26	48.1	10	6	ABR14084	Abr14084 Human can
25	26	48.1	10	6	ABR13509	Abr13509 Human can
26	26	48.1	10	6	ABR13884	Abr13884 Human can
27	26	48.1	10	6	ABR14551	Abr14551 Human can
28	26	48.1	10	6	ABR13906	Abr13906 Human can
29	26	48.1	10	6	ABR14106	Abr14106 Human can
30	26	48.1	10	6	ABR14337	Abr14337 Human can
31	26	48.1	10	6	ABR13701	Abr13701 Human can
32	26	48.1	10	6	ABR13151	Abr13151 Human can
33	26	48.1	13	2	AAY18293	Aay18293 Tendamist
34	26	48.1	13	7	ADO70271	Ado70271 Human mit
35	26	48.1	15	2	AAY18294	Aay18294 Tendamist
36	26	48.1	15	6	ABR33503	Abr33503 Human can
37	26	48.1	15	6	ABR33235	Abr33235 Human can
38	26	48.1	15	6	ABR33183	Abr33183 Human can
39	26	48.1	15	6	ABR33565	Abr33565 Human can
40	26	48.1	15	6	ABR33182	Abr33182 Human can
41	26	48.1	15	6	ABR33209	Abr33209 Human can
42	26	48.1	15	6	ABP71611	Abp71611 HSV-1 pep
43	25	46.3	7	8	ADN08728	Adn08728 Cotton wi
44	25	46.3	9	2	AAR37434	Aar37434 Promega p
45	25	46.3	9	2	AAW09657	Aaw09657 Labelled
46	25	46.3	10	4	AAB49007	Aab49007 Backbone
47	25	46.3	11	4	AAG70027	Aag70027 Human Chk
48	25	46.3	11	4	AAG68683	Aag68683 Human Chk
49	25	46.3	12	4	AAB89819	Aab89819 HIV gp120
50	25	46.3	12	4	AAB89818	Aab89818 HIV gp120

ALIGNMENTS

RESULT 1
AAB06265
ID AAB06265 standard; peptide; 11 AA.
XX
AC AAB06265;
XX
DT 03-OCT-2000 (first entry)
XX
DE Subtilisin-kexin SK-1 peptide substrate #1.
XX
KW Subtilisin-kexin isoenzyme 1; SKI-1; antilipaemic; cytostatic;
KW vasotropic; SKI-1 inhibitor; hypercholesterolaemia; liver steatosis;
KW Ras-dependent cancer; restenosis; amyloid protein formation;
KW pro-brain-derived neurotrophic factor; proBDNF.
XX
OS Synthetic.
XX
PN WO200026348-A2.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-CA001058.
XX
PR 04-NOV-1998; 98CA-02249648.
XX
PA (RECL-) INST RECH CLINIQUES MONTREAL.
XX
PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
XX
DR WPI; 2000-365601/31.
XX
PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence.
XX
PS Claim 26; Page 83; 119pp; English.
XX
CC The present sequence is a peptide which is capable of binding to and of
CC being cleaved by the subtilisin-kexin isoenzyme 1 (SKI-1) catalytic site.
CC SKI-1 is a type-1 membrane-bound proteinase which is highly conserved in
CC humans, mice and rats. SKI-1 cleaves at a specific threonine residue
CC within the N-terminal segment of human pro-brain-derived neurotrophic
CC factor (proBDNF). The present peptide may be used for monitoring SKI-1

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 17, 2005, 15:36:20 ; Search time 169 Seconds
(without alignments)
2400.492 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
Perfect score: 5537
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	5537	100.0	1052	9	US-09-891-711-4	Sequence 4, Appli
3	5537	100.0	1052	15	US-10-665-689-6	Sequence 6, Appli
4	5537	100.0	1052	16	US-10-829-118-4	Sequence 4, Appli
5	5537	100.0	1052	18	US-10-924-092A-208	Sequence 208, App
6	5537	100.0	1052	20	US-11-020-628-208	Sequence 208, App
7	5408	97.7	1052	9	US-09-891-711-6	Sequence 6, Appli
8	5408	97.7	1052	16	US-10-829-118-6	Sequence 6, Appli
9	3549	64.1	666	15	US-10-264-237-2631	Sequence 2631, Ap
10	2428	43.9	497	15	US-10-104-047-2347	Sequence 2347, Ap
11	1768.5	31.9	663	15	US-10-424-599-255271	Sequence 255271,
12	1664	30.1	2605	16	US-10-437-963-138449	Sequence 138449,
13	1467	26.5	280	18	US-10-924-092A-209	Sequence 209, App
14	1467	26.5	280	20	US-11-020-628-209	Sequence 209, App
15	663	12.0	224	16	US-10-767-701-55268	Sequence 55268, A
16	526	9.5	315	15	US-10-424-599-255270	Sequence 255270,
17	340	6.1	315	15	US-10-424-599-222557	Sequence 222557,
18	338.5	6.1	381	16	US-10-647-131-3	Sequence 3, Appli
19	338.5	6.1	381	16	US-10-647-131-4	Sequence 4, Appli
20	337.5	6.1	357	9	US-09-837-235-15	Sequence 15, Appl
21	337.5	6.1	357	20	US-11-043-731-15	Sequence 15, Appl
22	337.5	6.1	1139	14	US-10-156-761-10856	Sequence 10856, A
23	336.5	6.1	1079	14	US-10-112-488-39	Sequence 39, Appl
24	336.5	6.1	1079	16	US-10-673-860-8	Sequence 8, Appli
25	333.5	6.0	379	10	US-09-813-408-11	Sequence 11, Appl
26	333.5	6.0	381	16	US-10-647-131-2	Sequence 2, Appli
27	332.5	6.0	381	9	US-09-920-118-16	Sequence 16, Appl
28	331.5	6.0	379	9	US-09-920-118-14	Sequence 14, Appl
29	329	5.9	379	10	US-09-813-408-10	Sequence 10, Appl
30	329	5.9	379	15	US-10-146-905A-10	Sequence 10, Appl
31	329	5.9	380	15	US-10-146-905A-12	Sequence 12, Appl
32	326.5	5.9	275	14	US-10-324-152-22	Sequence 22, Appl
33	325	5.9	380	10	US-09-813-408-16	Sequence 16, Appl
34	324.5	5.9	275	14	US-10-324-152-6	Sequence 6, Appli
35	324.5	5.9	275	14	US-10-324-152-11	Sequence 11, Appl
36	324.5	5.9	275	17	US-10-872-166-14	Sequence 14, Appl
37	324.5	5.9	275	17	US-10-872-166-15	Sequence 15, Appl
38	324.5	5.9	275	17	US-10-873-917-11	Sequence 11, Appl
39	324.5	5.9	275	17	US-10-873-610-16	Sequence 16, Appl
40	324.5	5.9	275	17	US-10-872-162-11	Sequence 11, Appl
41	324.5	5.9	275	17	US-10-872-162-13	Sequence 13, Appl
42	324.5	5.9	276	17	US-10-873-917-14	Sequence 14, Appl
43	324	5.9	276	17	US-10-873-610-13	Sequence 13, Appl
44	323.5	5.8	275	8	US-08-322-678-8	Sequence 8, Appli
45	323.5	5.8	275	9	US-09-060-854B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-060-854B-7
; Sequence 7, Application US/09060854B
; Patent No. US20020081703A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David Aaron
; TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
; TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US20020C
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: GC532
; CURRENT APPLICATION NUMBER: US/09/060,854B
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-060-854B-7

Query Match 100.0%; Score 5537; DB 9; Length 1052;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFTAKARNSFISSA 60
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Db         17 GKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFTAKARNSFISSA 76

Qy         61 LKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQRKVFRSL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQRKVFRSL 136

Qy        121 KYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRRLLRAIPRQVAQT 180
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 17, 2005, 15:32:39 ; Search time 44 Seconds
(without alignments)
1757.646 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
Perfect score: 5537
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	5537	100.0	1052	3	US-09-360-237-3	Sequence 3, Appli
3	5537	100.0	1052	4	US-09-255-501-208	Sequence 208, App
4	5537	100.0	1052	4	US-09-060-854B-7	Sequence 7, Appli
5	5537	100.0	1052	4	US-09-891-711-4	Sequence 4, Appli
6	5537	100.0	1052	4	US-09-949-016-6413	Sequence 6413, Ap
7	5537	100.0	1052	4	US-09-060-872A-208	Sequence 208, App
8	5537	100.0	1052	4	US-09-500-135C-208	Sequence 208, App
9	5537	100.0	1058	4	US-09-949-016-10687	Sequence 10687, A
10	5408	97.7	1052	3	US-09-360-237-1	Sequence 1, Appli
11	5408	97.7	1052	4	US-09-891-711-6	Sequence 6, Appli
12	1467	26.5	280	4	US-09-255-501-209	Sequence 209, App
13	1467	26.5	280	4	US-09-060-872A-209	Sequence 209, App
14	1467	26.5	280	4	US-09-500-135C-209	Sequence 209, App
15	372.5	6.7	176	4	US-09-270-767-31702	Sequence 31702, A
16	338.5	6.1	352	1	US-07-923-260A-6	Sequence 6, Appli
17	337.5	6.1	352	1	US-07-923-260A-1	Sequence 1, Appli
18	337.5	6.1	381	1	US-07-772-087-5	Sequence 5, Appli
19	337.5	6.1	381	1	US-08-322-965-2	Sequence 2, Appli
20	330.5	6.0	275	1	US-07-864-298-1	Sequence 1, Appli
21	329	5.9	350	1	US-07-923-260A-4	Sequence 4, Appli
22	329	5.9	379	2	US-08-845-295A-1	Sequence 1, Appli
23	329	5.9	379	3	US-09-140-933-1	Sequence 1, Appli
24	329	5.9	379	3	US-09-146-661-1	Sequence 1, Appli
25	329	5.9	379	3	US-09-150-515-1	Sequence 1, Appli
26	327	5.9	378	1	US-07-772-087-4	Sequence 4, Appli
27	323.5	5.8	275	1	US-08-322-677A-8	Sequence 8, Appli
28	323.5	5.8	275	1	US-08-322-676-8	Sequence 8, Appli
29	323.5	5.8	275	3	US-08-898-218-8	Sequence 8, Appli
30	323.5	5.8	275	3	US-08-848-793-8	Sequence 8, Appli
31	323.5	5.8	275	3	US-09-255-502-3	Sequence 3, Appli
32	323.5	5.8	275	3	US-09-178-155-4	Sequence 4, Appli
33	323.5	5.8	275	3	US-09-445-270-3	Sequence 3, Appli
34	323.5	5.8	275	4	US-09-178-173A-4	Sequence 4, Appli
35	323.5	5.8	275	4	US-08-322-678-8	Sequence 8, Appli
36	323.5	5.8	275	4	US-09-255-501-4	Sequence 4, Appli
37	323.5	5.8	275	4	US-09-060-854B-4	Sequence 4, Appli
38	323.5	5.8	275	4	US-09-177-353-4	Sequence 4, Appli
39	323.5	5.8	275	4	US-10-033-325-4	Sequence 4, Appli
40	323.5	5.8	275	4	US-09-529-904-5	Sequence 5, Appli
41	323.5	5.8	275	4	US-09-060-872A-4	Sequence 4, Appli
42	323.5	5.8	275	4	US-09-500-135C-4	Sequence 4, Appli
43	323.5	5.8	275	6	5472855-4	Patent No. 5472855
44	323.5	5.8	275	6	5472855-4	Patent No. 5472855
45	323.5	5.8	352	1	US-07-923-260A-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-09-255-502-7
; Sequence 7, Application US/09255502
; Patent No. 6218165
; GENERAL INFORMATION:
;  APPLICANT:  Estell, David
;  APPLICANT:  Harding, Fiona
;  TITLE OF INVENTION:  Mutant Proteins Having Lower Allergenic Responses in
;  TITLE OF INVENTION:  Humans and Methods for Constructing, Identifying and
;  TITLE OF INVENTION:  Producing Such Proteins
;  FILE REFERENCE:  GC 527-D2
;  CURRENT APPLICATION NUMBER: US/09/255,502
;  CURRENT FILING DATE:  1999-02-23
;  PRIOR APPLICATION NUMBER:  09/060,872
;  PRIOR FILING DATE:  1998-04-15
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 1052
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-255-502-7

  Query Match           100.0%;  Score 5537;  DB 3;  Length 1052;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1036;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFTAKARNSFISSA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 GKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFTAKARNSFISSA 76

Qy         61 LKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQRKVFRSL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQRKVFRSL 136

Qy        121 KYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRRLLRAIPRQVAQT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 KYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRRLLRAIPRQVAQT 196

Qy        181 LQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGV 256

Qy        241 IASMRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNYAILKKIDVLNLSIGGPDFMDH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 IASMRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNYAILKKIDVLNLSIGGPDFMDH 316

Qy        301 PFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 PFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMT 376
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 17, 2005, 15:31:04 ; Search time 183 Seconds
(without alignments)
2898.984 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
Perfect score: 5537
Sequence: 1 GKKHLGDRLEKKSPEKAPCP.....PRVKRPQLMQQVHPPKTPSV 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5537	100.0	1052	1	MS1P_HUMAN	Q14703 homo sapien
2	5408	97.7	1052	1	MS1P_CRIGR	Q9z2a8 cricetulus
3	5396	97.5	1052	1	MS1P_RAT	Q9wtz3 rattus norv
4	5360	96.8	1052	1	MS1P_MOUSE	Q9wtz2 mus musculu
5	5357	96.7	1052	2	Q6PG67	Q6pg67 mus musculu
6	5339	96.4	1055	2	Q80U80	Q80u80 mus musculu
7	4770	86.1	1074	2	Q6X1U1	Q6x1u1 brachydanio
8	4522	81.7	950	2	Q6AX98	Q6ax98 xenopus lae
9	2835	51.2	552	2	Q8TAN4	Q8tan4 homo sapien
10	2815.5	50.8	1238	2	Q7PVB0	Q7pvb0 anopheles g
11	2377.5	42.9	1012	2	Q9VP10	Q9vp10 drosophila
12	2269	41.0	1038	2	Q8L7B7	Q8l7b7 arabidopsis
13	355	6.4	1239	2	Q9FBZ4	Q9fbz4 streptomyce
14	346.5	6.3	1722	2	Q9NDZ2	Q9ndz2 leishmania
15	339.5	6.1	381	2	Q84F18	Q84f18 bacillus su
16	338.5	6.1	381	1	SUBN_BACNA	P35835 bacillus su
17	338.5	6.1	381	1	SUBT_BACSA	P00783 bacillus su
18	338.5	6.1	381	1	SUBT_BACST	P29142 bacillus st
19	337.5	6.1	381	1	SUBT_BACSU	P04189 bacillus su
20	337.5	6.1	1139	2	Q82I39	Q82i39 streptomyce
21	336	6.1	1102	2	P95684	P95684 streptomyce
22	335.5	6.1	1245	2	Q9RL54	Q9rl54 streptomyce
23	333.5	6.0	379	2	Q9FDF4	Q9fdf4 bacillus li
24	333.5	6.0	379	2	Q65LP7	Q65lp7 bacillus li
25	333.5	6.0	381	2	Q847A2	Q847a2 bacillus su
26	329	5.9	379	1	SUBT_BACLI	P00780 bacillus li
27	327.5	5.9	627	2	Q9RUD0	Q9rud0 deinococcus
28	322	5.8	382	2	Q45522	Q45522 bacillus sp
29	321	5.8	379	2	Q45301	Q45301 bacillus li
30	321	5.8	379	2	Q6BCN9	Q6bcn9 bacillus mo
31	321	5.8	379	2	Q6PNN5	Q6pnn5 bacillus li
32	320.5	5.8	275	2	Q93L66	Q93166 bacillus su
33	320.5	5.8	379	2	Q45300	Q45300 bacillus li
34	320	5.8	1105	2	Q8KKH6	Q8kkh6 streptomyce
35	318.5	5.8	374	2	Q9F942	Q9f942 bacillus li
36	318.5	5.8	381	2	Q7WVA6	Q7wva6 bacillus su
37	318.5	5.8	382	1	SUBT_BACAM	P00782 bacillus am
38	318	5.7	374	2	Q9F943	Q9f943 bacillus li
39	317	5.7	379	2	Q53521	Q53521 bacillus li
40	316.5	5.7	275	1	SUBT_BACPU	P07518 bacillus pu
41	316.5	5.7	382	2	Q6IT79	Q6it79 bacillus sp
42	316	5.7	374	2	Q9F941	Q9f941 bacillus li
43	314.5	5.7	312	2	Q93QZ0	Q93qz0 clostridium
44	314	5.7	404	2	Q76L29	Q76l29 bacillus sp
45	314	5.7	1237	2	Q8GGT4	Q8ggt4 streptomyce

ALIGNMENTS

RESULT 1
MS1P_HUMAN
ID MS1P_HUMAN STANDARD; PRT; 1052 AA.
AC Q14703; Q9UF67;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Membrane-bound transcription factor site-1 protease precursor
DE (EC 3.4.21.-) (Site-1 protease) (Subtilisin/kexin-isozyme-1) (SKI-1).
GN Name=MBTPS1; Synonyms=KIAA0091, S1P, SKI1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid;
RX MEDLINE=20401147; PubMed=10944850;
RA Nakajima T., Iwaki K., Kodama T., Inazawa J., Emi M.;
RT "Genomic structure and chromosomal mapping of the human site-1
RT protease (S1P) gene.";
RL J. Hum. Genet. 45:212-217(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. III.
RT The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 2:37-43(1995).
RN [3]
RP SEQUENCE OF 735-1052 FROM N.A.
RC TISSUE=Testis;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP CHARACTERIZATION, PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=20112790; PubMed=10644685; DOI=10.1074/jbc.275.4.2349;
RA Toure B.B., Munzer J.S., Basak A., Benjannet S., Rochemont J.,
RA Lazure C., Chretien M., Seidah N.G.;
RT "Biosynthesis and enzymatic characterization of human SKI-1/S1P and
RT the processing of its inhibitory prosegment.";
RL J. Biol. Chem. 275:2349-2358(2000).
RN [5]
RP SUBCELLULAR LOCATION.
RX MEDLINE=99145548; PubMed=9990022; DOI=10.1073/pnas.96.4.1321;
RA Seidah N.G., Mowla S.J., Hamelin J., Mamarbachi A.M., Benjannet S.,
RA Toure B.B., Basak A., Munzer J.S., Marcinkiewicz J., Zhong M.,
RA Barale J.-C., Lazure C., Murphy R.A., Chretien M., Marcinkiewicz M.;
RT "Mammalian subtilisin/kexin isozyme SKI-1: a widely expressed
RT proprotein convertase with a unique cleavage specificity and cellular
RT localization.";

OM protein - protein search, using sw model

Run on: August 17, 2005, 15:19:31 ; Search time 48 Seconds
(without alignments)
2076.678 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
Perfect score: 5537
Sequence: 1 GKKHLGDRLEKKSFEKAPCP.....PRVKRPQLMQQVHPPKTPSV 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5408	97.7	1052	2	T17093	intraluminal subti
2	1716	31.0	318	2	T43492	hypothetical prote
3	338.5	6.1	381	1	SUBSS	subtilisin (EC 3.4
4	338.5	6.1	381	2	JQ1487	subtilisin (EC 3.4
5	338.5	6.1	381	2	JH0778	subtilisin (EC 3.4
6	337.5	6.1	381	1	SUBSI	subtilisin (EC 3.4
7	329	5.9	379	1	SUBSCL	subtilisin (EC 3.4
8	327.5	5.9	627	2	D75393	serine proteinase,
9	322	5.8	382	2	I39780	subtilisin (EC 3.4
10	318.5	5.8	382	1	SUBSN	subtilisin (EC 3.4
11	312.5	5.6	272	2	A23624	subtilisin (EC 3.4
12	308	5.6	274	1	SUBSD	subtilisin (EC 3.4
13	304.5	5.5	323	2	I39867	microbial serine p
14	299	5.4	326	1	C41335	microbial serine p
15	295	5.3	275	2	JC1085	subtilisin (EC 3.4
16	294	5.3	321	2	JC5460	intracellular alka
17	293.5	5.3	322	2	G83922	intracellular alka
18	289	5.2	319	2	I39866	microbial serine p
19	285.5	5.2	374	2	I39781	subtilisin (EC 3.4
20	284.5	5.1	321	1	S27501	alkaline proteinas
21	283	5.1	380	2	A49778	high-alkaline seri
22	281.5	5.1	1398	2	T28159	pyrolysin (EC 3.4.
23	271	4.9	384	2	JC4802	alkaline proteinas
24	270.5	4.9	328	2	G95392	probable protease
25	266	4.8	378	2	A33973	high-alkaline seri
26	260.5	4.7	682	2	S44131	subtilisin-like pr
27	257	4.6	1448	2	AI2007	Subtilase family p
28	256	4.6	757	2	C84120	subtilisin-type pr
29	253	4.6	397	2	JW0075	cysteine-dependent
30	251.5	4.5	436	2	I39973	alkaline serine pr
31	250	4.5	442	2	A69587	intracellular alka
32	249.5	4.5	1345	2	T29090	surface layer-asso
33	249	4.5	806	2	A41341	microbial serine p
34	246	4.4	1331	2	A72647	probable surface l
35	243.5	4.4	401	2	A57690	aerolysin precurso
36	243	4.4	645	1	SUBSMP	serine proteinase
37	242	4.4	419	1	S25835	subtilisin (EC 3.4
38	241.5	4.4	412	2	T42024	probable serine pr
39	241.5	4.4	420	1	S23407	subtilisin (EC 3.4
40	241.5	4.4	792	2	H83736	subtilisin-type al
41	240	4.3	401	2	I39974	serine proteinase
42	239	4.3	444	2	B83891	intracellular alka
43	235	4.2	488	2	AI1930	proteinase [import
44	231.5	4.2	799	2	G83753	subtilisin-type pr
45	230.5	4.2	361	2	G83756	subtilisin-type al

ALIGNMENTS

RESULT 1
T17093
intraluminal subtilisin-like proteinase S1P, membrane-bound - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T17093
R;Sakai, J.; Rawson, R.B.; Espenshade, P.J.; Cheng, D.; Seegmiller, A.C.; Goldstein, J.
Molecular Cell 2, 505-514, 1998
A;Title: Molecular identification of the sterol-regulated luminal protease that cleaves
A;Reference number: Z18677; MUID:99026600; PMID:9809072
A;Accession: T17093
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1052 <SAK>
A;Cross-references: UNIPROT:Q9Z2A8; EMBL:AF078105; NID:g3892203; PID:g3892204; PIDN:AAC
A;Experimental source: strain 25-RA
C;Function:
A;Description: S1P is proposed to be a sterol-regulated protease that controls lipid me
A;Note: S1P cleaves sterol regulatory element binding proteins (SREBPs) in the ER lumin

Query Match 97.7%; Score 5408; DB 2; Length 1052;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1006; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 GKKHLGDRLEKKSFEKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFTAKARNSFISSA 60
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Db         17 GKKHLGDRLGKKAFEKASCPSCSHLTLKVEFSSTVVEYEYIVAFNGYFTAKARNSFISSA 76

Qy         61 LKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQRKVFRSL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LKSSEVDNWRIIPRNNPSSDYPSDFEVIQIKEKQKAGLLTLEDHPNIKRVTPQRKVFRSL 136

Qy        121 KYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRRLLRAIPRQVAQT 180
              |:||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 KFAESDPIVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRRLLRAIPRQVAQT 196

Qy        181 LQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LQADVLWQMGYTGANVRVAVFDTGLSEKHPHFKNVKERTNWTNERTLDDGLGHGTFVAGV 256

Qy        241 IASMRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNYAILKKIDVLNLSIGGPDFMDH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 IASMRECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNYAILKKIDVLNLSIGGPDFMDH 316

Qy        301 PFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 PFVDKVWELTANNVIMVSAIGNDGPLYGTLNNPADQMDVIGVGGIDFEDNIARFSSRGMT 376

Qy        361 TWELPGGYGRMKPDIVTYGAGVRGSGVKGGCRALSGTSVASPVVAGAVTLLVSTVQKREL 420
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 TWELPGGYGRVKPDIVTYGAGVRGSGVKGGCRALSGTSVASPVVAGAVTLLVSTVQKREL 436
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 17, 2005, 15:18:18 ; Search time 169 Seconds
(without alignments)
2370.910 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
Perfect score: 5537
Sequence: 1 GKKHLGDRLEKKSFEKAPCP.....PRVKRPQLMQQVHPPKTPSV 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5537	100.0	1052	3	AAB06334	Aab06334 Human sub
2	5537	100.0	1052	3	AAY54619	Aay54619 Human sub
3	5537	100.0	1052	3	AAY66982	Aay66982 Human sub
4	5537	100.0	1052	3	AAY84227	Aay84227 Amino aci
5	5537	100.0	1052	4	AAU38520	Aau38520 Human sub
6	5537	100.0	1052	5	AAE14527	Aae14527 Human sit
7	5537	100.0	1052	5	ABG91096	Abg91096 Human sub
8	5408	97.7	1052	3	AAY84228	Aay84228 Amino aci
9	5408	97.7	1052	5	AAE14528	Aae14528 Hamster s
10	5396	97.5	1052	3	AAB06335	Aab06335 Rat subti
11	5360	96.8	1052	3	AAB06336	Aab06336 Mouse sub
12	3549	64.1	666	5	ABB90255	Abb90255 Human pol
13	2428	43.9	497	7	ADB64193	Adb64193 Human pro
14	2366.5	42.7	992	4	AAB20015	Aab20015 Drosophil
15	2231	40.3	952	4	ABB63047	Abb63047 Drosophil
16	606	10.9	129	5	ADK34880	Adk34880 Novel hum
17	585	10.6	125	5	ADK36735	Adk36735 Novel hum
18	463	8.4	126	4	AAO01619	Aao01619 Human pol
19	343.5	6.2	392	6	ABP59571	Abp59571 Protein a
20	340.5	6.1	381	1	AAP60571	Aap60571 Sequence
21	340.5	6.1	381	1	AAP80744	Aap80744 Sequence
22	340.5	6.1	381	2	AAR07970	Aar07970 Substilin
23	338.5	6.1	352	2	AAW46600	Aaw46600 Suppresso
24	338.5	6.1	387	6	ABP59567	Abp59567 Protein a
25	338.5	6.1	388	6	ABP59569	Abp59569 Protein a
26	338.5	6.1	400	6	ABP59565	Abp59565 Protein a
27	337.5	6.1	352	2	AAW46595	Aaw46595 Amino aci
28	337.5	6.1	381	1	AAP71060	Aap71060 Wild-type
29	337.5	6.1	381	2	AAR03737	Aar03737 Subtilisi
30	337.5	6.1	381	2	AAR24131	Aar24131 Bacterial
31	337.5	6.1	381	2	AAR34463	Aar34463 Bacillus
32	337.5	6.1	381	2	AAR74224	Aar74224 B.subtili
33	337.5	6.1	381	2	AAY39229	Aay39229 Bacillus
34	336.5	6.1	381	1	AAP70053	Aap70053 Bacillus
35	336.5	6.1	1079	4	AAB81180	Aab81180 Transglut
36	336.5	6.1	1079	6	ABU07391	Abu07391 Foreign p
37	333.5	6.0	275	2	AAR51928	Aar51928 Bacillus
38	333.5	6.0	379	6	AAE29944	Aae29944 Bacillus
39	332.5	6.0	381	5	AAE19063	Aae19063 Bacillus
40	331.5	6.0	379	5	AAE19062	Aae19062 Bacillus
41	330.5	6.0	275	2	AAR52643	Aar52643 Bacillus
42	330.5	6.0	275	2	AAR51924	Aar51924 Bacillus
43	330.5	6.0	275	2	AAR51929	Aar51929 Bacillus
44	330.5	6.0	275	2	AAR51920	Aar51920 Bacillus
45	329.5	6.0	275	2	AAR51927	Aar51927 Bacillus

ALIGNMENTS

RESULT 1
AAB06334
ID AAB06334 standard; protein; 1052 AA.
XX
AC AAB06334;
XX
DT 03-OCT-2000 (first entry)
XX
DE Human subtilisin-kexin isoenzyme 1.
XX
KW Human; subtilisin-kexin isoenzyme 1; SKI-1; antilipaemic; cytostatic;
KW vasotropic; SKI-1 inhibitor; hypercholesterolaemia; liver steatosis;
KW Ras-dependent cancer; restenosis; amyloid protein formation;
KW pro-brain-derived neurotrophic factor; proBDNF;
KW sterol-regulatory element-binding protein; SREBP.
XX
OS Homo sapiens.
XX
PN WO200026348-A2.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-CA001058.
XX
PR 04-NOV-1998; 98CA-02249648.
XX
PA (RECL-) INST RECH CLINIQUES MONTREAL.
XX
PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
XX
DR WPI; 2000-365601/31.
DR N-PSDB; AAA57197.
XX
PT Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
PT producing a polypeptide useful for treating hypercholesterolemia, liver
PT steatosis and amyloidosis, comprises a specific amino acid sequence.
XX
PS Claim 1; Page 56-59; 119pp; English.
XX
CC The present sequence is human subtilisin-kexin isoenzyme 1 (SKI-1), a
CC type-1 membrane-bound proteinase. The nucleotide sequence was isolated
CC from the human neuronal cell line IMR-32 by RT-PCR using active site
CC degenerate primers. SKI-1 cleaves at a specific threonine residue within
CC the N-terminal segment of human pro-brain-derived neurotrophic factor
CC (proBDNF). It is also capable of cleaving sterol-regulatory element-
CC binding proteins (SREBPs), which function to control lipid biosynthesis
CC and uptake in animal cells. Peptides which bind to and are cleaved by SKI
CC -1 may be used for monitoring SKI-1 activity, for screening inhibitors of